

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 31-Mar-1997

(C) CLASSIFICATION:

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30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/625328

(B) FILING DATE: 1-Apr-1996

(vii) PRIOR APPLICATION DATA:

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(A) APPLICATION NUMBER: 08/710802

(B) FILING DATE: 23-Sep-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1007P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30
Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
35 40 45
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60
Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
5 95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
10 125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
140 145 150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
15 155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
20 170 175 180

Thr
181

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: Nucleic Acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
 TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTCG AGAGGCTGCC 100
 5 CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150
 ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200
 TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
 10 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
 15 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
 ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30 CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

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GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
5 AGATTGGTCT GTTTTGTTCG AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600
AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCTG 650
10 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
20 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACCTTCA GCCAGCATTC 1150
30 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
35 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300

ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
 5 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 417 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
 1 5 10 15
 20 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
 20 25 30
 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
 35 40 45
 25 Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
 50 55 60
 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
 65 70 75
 30 Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
 80 85 90
 Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
 35 95 100 105

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Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	110	115	120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro	125	130	135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His	140	145	150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys	155	160	165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	170	175	180
Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	185	190	195
Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	200	205	210
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg	215	220	225
His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	230	235	240
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	245	250	255
Asp	Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	260	265	270
Ile	Cys	Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	275	280	285

	Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	
					290					295					300	
5	Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	
					305					310					315	
	Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	
					320					325					330	
10	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg	
					335					340					345	
	Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu	
					350					355					360	
15	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Gly	Arg	Phe	Arg	Asp	Gln	Gln	
					365					370					375	
	Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu	
20					380					385					390	
	Gly	Ala	Val	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gly	Cys	
					395					400					405	
25	Val	Glu	Asp	Leu	Arg	Ser	Arg	Leu	Gln	Arg	Gly	Pro				
					410					415		417				

(2) INFORMATION FOR SEQ ID NO:7:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

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(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1634 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94

Met Glu

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CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
 5 10 15

5 CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
 20 25

10 CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
 30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGC 250
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
 45 50

CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
 55 60 65

TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 70 75 80

25 TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
 85 90

30 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn
 95 100 105

35 TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro
 110 115

GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484
 Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser
 120 125 130

5 AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523
 Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
 135 140 145

10 GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562
 Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg
 150 155

15 GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601
 Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu
 160 165 170

20 CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640
 His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu
 175 180

25 GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679
 Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp
 185 190 195

30 AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718
 Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu
 200 205 210

35 GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757
 Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr
 215 220

TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796
 Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala
 225 230 235

GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835
 Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala
 240 245

5 ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874
 Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu
 250 255 260

10 GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913
 Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln
 265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952
 Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
 280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
 290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
 Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro
 305 310

25 ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
 Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
 315 320 325

30 ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108
 Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp
 330 335 340

35 GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
 Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
 345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186
 Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val
 355 360 365

5 GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
 Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
 370 375

10 AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
 Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
 380 385 390

15 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
 Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
 395 400 405

20 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
 Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
 410 415 417

25 GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

30 GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30